



SEQUENCE LISTING

<110> Loughney, Kate

<120> Phosphodiesterase 10

<130> 27866/38275

<140> 10/083,620

<141> 2002-02-26

<150> 09/256,000

<151> 1999-02-23

<150> 60/075,508

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<170> PatentIn Ver. 2.0

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Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
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atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc 148
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
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aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta 196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
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gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 244
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
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tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
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agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag 340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
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aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc 388
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
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tct cca gag acc atc gag gcc ctg cgg aag cgg acc ttt gac gtc tgg 436
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
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Phe	Lys	Gln	Ile	Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp					
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 ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag 1252
 Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
 395 400 405
 gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag 1300
 Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
 410 415 420 425
 ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac 1348
 Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
 430 435 440
 agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat 1396
 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
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 Val Lys Asn Ser Glu Gly Asp Cys Ala
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 Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
 50 55 60
 Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
 65 70 75 80
 Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
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 Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
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 Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
 115 120 125
 Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
 130 135 140
 Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
 145 150 155 160

Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
 165 170 175
 Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
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 Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
 195 200 205
 Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
 210 215 220
 His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
 225 230 235 240
 Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
 245 250 255
 His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
 260 265 270
 Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
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 305 310 315 320
 Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
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 Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
 355 360 365
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 Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
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 Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
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 Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
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gtgaccaagn tcttccccat ggttgaggag atcatgctgc agccactttg ggaatcccga 180
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ccaacatccc acctgatggg ttcaagcaga tccgacag 158

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ttcccgtggc cccgttcattg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tcccaatggt tgaaacagtg accaagctct tccccatggg 240

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 gcagcatgat cttcctcaac catggggggg aggagcttgg ggcactngtt ttcaaaaatt 360
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ccagaactgc agccacgccc cccgttttcc tcaggcacag tctccttcac tgtttttcac 180
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gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagttt 360
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tgggggntgt gggccttg 438

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ttactggaag aatattttat gcagagtgc cgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga cgagacaaa gtgaccaaag caacagccca aattgggttc atcaagtttg 240
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ttactggaag aatattttat gcagagtgc cgtgagaagt ccgaagcctt cctgtggccc 180
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                                Cys His Cys Leu Leu His
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tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg 164
Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
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ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc 212
Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
                        25                      30                     35

atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc 260
Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
                        40                      45                     50

ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat 308
Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
                    55                      60                     65                      70
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cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag 356
 Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
 75 80 85
 aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag 404
 Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
 90 95 100
 aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 453
 Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala
 105 110 115
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 Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro
 50 55 60
 Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp
 65 70 75 80
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 <213> Artificial Sequence

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<222> (107)..(1066)

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 Ala Leu Glu
 1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163
 His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro
 5 10 15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
 Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
 20 25 30 35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259
 Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
 40 45 50

tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg 307
 Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
 55 60 65

gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat 355
 Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His
 70 75 80

ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg gcg 403
 Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala
 85 90 95

gtc cgc tac aat gac atc tca ccg ctg gag aac cac cac tgc gcc gtg 451
 Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val
 100 105 110 115

gcc ttc cag atc ctc gcc gag cct gag tgc aac atc ttc tcc aac atc 499
 Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile
 120 125 130

cca cct gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc 547
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 Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu
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 ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt 691
 Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg
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 cca atg gaa gtc gca gag cct tgg gtg gac tgt tta tta gag gaa tat 739
 Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr
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 Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
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 Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
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 Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
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 Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
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 Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
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 Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu
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<211> 1887

<212> DNA

<213> Homo sapiens

<220>

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<222> (74)..(1672)

<400> 18

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Ile Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys
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Tyr Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly
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Leu Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met
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aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta 445
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gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 493
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
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tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 541
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
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Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
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aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc 637
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
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tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg 685
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
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Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His
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gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg 781
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Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile		
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Leu	Ile	Lys	Cys	Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val		
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Asp	Arg	Glu	Lys	Ser	Glu	Gly	Leu	Pro	Val	Ala	Pro	Phe	Met	Asp	Arg		
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 Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
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 Val Lys Asn Ser Glu Gly Asp Cys Ala
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 35 40 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
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Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
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Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
 85 90 95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
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Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
 115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
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Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
 145 150 155 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
 165 170 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
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 Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
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 Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
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 Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240
 Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
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 Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
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 Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
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 Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
 355 360 365
 Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
 370 375 380
 Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
 385 390 395 400
 Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
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 Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
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 Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
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 Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
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 Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
 485 490 495
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Glu Gly Asp Cys Ala
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Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
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cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc 145
Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
35 40 45

tcc atc gac ccc acc atg ccc gcg aat tca gaa cgc act ccg tac aaa 193
Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
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gtg aga cct gtg gcc atc aag caa ctc tcc gct gat gtc gag gac aag 241
Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

aga acc aca agc cgt ggc cag tct gct gag aga cca ctg agg gac aga 289
Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
85 90 95

cgg gtt gtg ggc ctg gag cag ccc cgg agg gaa gga gca ttt gaa agt 337
Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
100 105 110

gga cag gta gag ccc agg ccc aga gag ccc cag ggc tgc tac cag gaa 385
Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
115 120 125

ggc cag cgc atc cct cca gag aga gaa gaa tta atc cag agc gtg ctg 433
Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
130 135 140

gcg cag gtt gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg 481
Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
145 150 155 160

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Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

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Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile

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Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu					
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Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His	Ala					
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gaa	att	atg	gat	tct	ttc	aaa	gag	aaa	atg	gag	aat	ttt	gac	tac	agc	1297				
Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr	Ser					
			420					425					430							
aac	gag	gag	cac	atg	acc	ctg	ctg	aag	atg	att	ttg	ata	aaa	tgc	tgt	1345				

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
 435 440 445
 gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg 1393
 Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
 450 455 460
 gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca 1441
 Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
 465 470 475 480
 gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag 1489
 Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
 485 490 495
 gcc aca gcc cag att ggg ttc atc aag ttt gtc ctg atc cca atg ttt 1537
 Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
 500 505 510
 gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag 1585
 Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
 515 520 525
 cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cgg ata gat 1633
 Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
 530 535 540
 gac gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg 1681
 Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
 545 550 555 560
 gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa 1729
 Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
 565 570 575
 gga gac tgt gcc tgaggaaagc ggggggcgtg gctgcagttc tggacgggct 1781
 Gly Asp Cys Ala
 580
 ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc ctgggcacct ggcaccacaa 1841
 gaccatgttt tctaagaacc attttgttca ctgatacaaaa aaaaaaaaaa ggaattcatg 1901
 atgctgtaca gaattttatt tttaaactgt cttttaaata atatattctt atacggaaaa 1961
 aaaaaa 1967

 <210> 21
 <211> 580
 <212> PRT
 <213> Homo sapiens

 <400> 21
 Tyr Leu Asp Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr
 1 5 10 15
 Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu
 20 25 30
 Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val
 35 40 45

Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
 50 55 60
 Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
 65 70 75 80
 Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg
 85 90 95
 Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser
 100 105 110
 Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu
 115 120 125
 Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu
 130 135 140
 Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu
 145 150 155 160
 Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
 165 170 175
 Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile
 180 185 190
 Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys
 195 200 205
 Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg
 210 215 220
 Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile
 225 230 235 240
 Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn
 245 250 255
 Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val
 260 265 270
 Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys
 275 280 285
 Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
 290 295 300
 Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
 305 310 315 320
 Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
 325 330 335
 Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile
 340 345 350
 Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
 355 360 365
 Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
 370 375 380

Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
 385 390 395 400
 Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
 405 410 415
 Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
 420 425 430
 Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
 435 440 445
 Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
 450 455 460
 Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
 465 470 475 480
 Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
 485 490 495
 Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
 500 505 510
 Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
 515 520 525
 Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
 530 535 540
 Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
 545 550 555 560
 Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
 565 570 575
 Gly Asp Cys Ala
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<210> 22
 <211> 1457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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<400> 22
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 ggaaagtaca gtaaaaagtc cgagtgcagc cgccggggcgc agg atg gga tcc ggc 175
 Met Gly Ser Gly
 1
 tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc 223
 Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg
 5 10 15 20
 att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271

Ile	Gln	Lys	Val	Ile	Phe	Ser	Lys	Tyr	Cys	Asn	Ser	Ser	Asp	Ile	Met		
				25					30					35			
gac	ctg	ttc	tgc	atc	gcc	acc	ggc	ctg	cct	cgg	aac	acg	acc	atc	tcc	319	
Asp	Leu	Phe	Cys	Ile	Ala	Thr	Gly	Leu	Pro	Arg	Asn	Thr	Thr	Ile	Ser		
			40					45					50				
ctg	ctg	acc	acc	gac	gac	gcc	atg	gtc	tcc	atc	gac	ccc	acc	atg	ccc	367	
Leu	Leu	Thr	Thr	Asp	Asp	Ala	Met	Val	Ser	Ile	Asp	Pro	Thr	Met	Pro		
		55					60					65					
gcg	aat	tca	gaa	cgc	act	ccg	tac	aaa	gtg	aga	cct	gtg	gcc	atc	aag	415	
Ala	Asn	Ser	Glu	Arg	Thr	Pro	Tyr	Lys	Val	Arg	Pro	Val	Ala	Ile	Lys		
	70					75					80						
caa	ctc	tcc	gag	aga	gaa	gaa	tta	atc	cag	agc	gtg	ctg	gcg	cag	gtt	463	
Gln	Leu	Ser	Glu	Arg	Glu	Glu	Leu	Ile	Gln	Ser	Val	Leu	Ala	Gln	Val		
	85				90					95					100		
gca	gag	cag	ttc	tca	aga	gca	ttc	aaa	atc	aat	gaa	ctg	aaa	gct	gaa	511	
Ala	Glu	Gln	Phe	Ser	Arg	Ala	Phe	Lys	Ile	Asn	Glu	Leu	Lys	Ala	Glu		
				105					110					115			
gtt	gca	aat	cac	ttg	gct	gtc	cta	gag	aaa	cgc	gtg	gaa	ttg	gaa	gga	559	
Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val	Glu	Leu	Glu	Gly		
			120					125					130				
cta	aaa	gtg	gtg	gag	att	gag	aaa	tgc	aag	agt	gac	att	aag	aag	atg	607	
Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp	Ile	Lys	Lys	Met		
		135					140					145					
agg	gag	gag	ctg	gcg	gcc	aga	agc	agc	agg	acc	aac	tgc	ccc	tgt	aag	655	
Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn	Cys	Pro	Cys	Lys		
	150					155					160						
tac	agt	ttt	ttg	gat	aac	cac	aag	aag	ttg	act	cct	cga	cgc	gat	gtt	703	
Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro	Arg	Arg	Asp	Val		
	165				170					175					180		
ccc	act	tac	ccc	aag	tac	ctg	ctc	tct	cca	gag	acc	atc	gag	gcc	ctg	751	
Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr	Ile	Glu	Ala	Leu		
				185					190					195			
cgg	aag	ccg	acc	ttt	gac	gtc	tgg	ctt	tgg	gag	ccc	aat	gag	atg	ctg	799	
Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro	Asn	Glu	Met	Leu		
			200				205						210				
agc	tgc	ctg	gag	cac	atg	tac	cac	gac	ctc	ggg	ctg	gtc	agg	gac	ttc	847	
Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu	Val	Arg	Asp	Phe		
		215					220					225					
agc	atc	aac	cct	gtc	acc	ctc	agg	agg	tgg	ctg	ttc	tgc	gtc	cac	gac	895	
Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe	Cys	Val	His	Asp		
	230					235					240						
aac	tac	aga	aac	aac	ccc	ttc	cac	aac	ttc	cgg	cac	tgc	ttc	tgc	gtg	943	
Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His	Cys	Phe	Cys	Val		
	245				250					255					260		
gcc	cag	atg	atg	tac	agc	atg	gtc	tgg	ctc	tgc	agt	ctc	cag	gag	aag	991	
Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser	Leu	Gln	Glu	Lys		
				265					270					275			

ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc atc tgc cac 1039
 Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His
 280 285 290
 gat ctg gac cat ccc ggc tac aac aac acg tac cag atc aat gcc cgc 1087
 Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg
 295 300 305
 aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg gag aac cac 1135
 Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His
 310 315 320
 cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag tgc aac atc 1183
 His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile
 325 330 335 340
 ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga cag gga atg 1231
 Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met
 345 350 355
 atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg 1279
 Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met
 360 365 370
 gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag 1327
 Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu
 375 380 385
 cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct 1375
 His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser
 390 395 400
 aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta 1423
 Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu
 405 410 415 420
 tta gag gaa tat ttt atg cag agc gac cgt gaga 1457
 Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
 425 430

<210> 23
 <211> 430
 <212> PRT
 <213> Homo sapiens

<400> 23
 Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
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 Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
 20 25 30
 Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
 35 40 45
 Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60
 Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
 65 70 75 80
 Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val

85										90				95			
Leu	Ala	Gln	Val	Ala	Glu	Gln	Phe	Ser	Arg	Ala	Phe	Lys	Ile	Asn	Glu		
			100					105					110				
Leu	Lys	Ala	Glu	Val	Ala	Asn	His	Leu	Ala	Val	Leu	Glu	Lys	Arg	Val		
		115					120					125					
Glu	Leu	Glu	Gly	Leu	Lys	Val	Val	Glu	Ile	Glu	Lys	Cys	Lys	Ser	Asp		
		130				135					140						
Ile	Lys	Lys	Met	Arg	Glu	Glu	Leu	Ala	Ala	Arg	Ser	Ser	Arg	Thr	Asn		
145					150					155					160		
Cys	Pro	Cys	Lys	Tyr	Ser	Phe	Leu	Asp	Asn	His	Lys	Lys	Leu	Thr	Pro		
				165					170					175			
Arg	Arg	Asp	Val	Pro	Thr	Tyr	Pro	Lys	Tyr	Leu	Leu	Ser	Pro	Glu	Thr		
			180					185					190				
Ile	Glu	Ala	Leu	Arg	Lys	Pro	Thr	Phe	Asp	Val	Trp	Leu	Trp	Glu	Pro		
		195					200					205					
Asn	Glu	Met	Leu	Ser	Cys	Leu	Glu	His	Met	Tyr	His	Asp	Leu	Gly	Leu		
		210				215					220						
Val	Arg	Asp	Phe	Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Arg	Trp	Leu	Phe		
225					230					235					240		
Cys	Val	His	Asp	Asn	Tyr	Arg	Asn	Asn	Pro	Phe	His	Asn	Phe	Arg	His		
				245					250					255			
Cys	Phe	Cys	Val	Ala	Gln	Met	Met	Tyr	Ser	Met	Val	Trp	Leu	Cys	Ser		
			260					265					270				
Leu	Gln	Glu	Lys	Phe	Ser	Gln	Thr	Asp	Ile	Leu	Ile	Leu	Met	Thr	Ala		
		275					280					285					
Ala	Ile	Cys	His	Asp	Leu	Asp	His	Pro	Gly	Tyr	Asn	Asn	Thr	Tyr	Gln		
		290				295					300						
Ile	Asn	Ala	Arg	Thr	Glu	Leu	Ala	Val	Arg	Tyr	Asn	Asp	Ile	Ser	Pro		
305					310					315					320		
Leu	Glu	Asn	His	His	Cys	Ala	Val	Ala	Phe	Gln	Ile	Leu	Ala	Glu	Pro		
				325					330					335			
Glu	Cys	Asn	Ile	Phe	Ser	Asn	Ile	Pro	Pro	Asp	Gly	Phe	Lys	Gln	Ile		
			340					345					350				
Arg	Gln	Gly	Met	Ile	Thr	Leu	Ile	Leu	Ala	Thr	Asp	Met	Ala	Arg	His		
		355					360					365					
Ala	Glu	Ile	Met	Asp	Ser	Phe	Lys	Glu	Lys	Met	Glu	Asn	Phe	Asp	Tyr		
		370				375					380						
Ser	Asn	Glu	Glu	His	Met	Thr	Leu	Leu	Lys	Met	Ile	Leu	Ile	Lys	Cys		
385					390					395					400		
Cys	Asp	Ile	Ser	Asn	Glu	Val	Arg	Pro	Met	Glu	Val	Ala	Glu	Pro	Trp		
				405					410					415			
Val	Asp	Cys	Leu	Leu	Glu	Glu	Tyr	Phe	Met	Gln	Ser	Asp	Arg				

<210> 24
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FLAG epitope

<400> 24
Asp Thr Lys Asp Asp Asp Asp Lys
1 5

<210> 25
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 25
tagaccatgg actacaagga cgacgatgac aagatggacg cattcagaag cact 54

<210> 26
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 26
cgaggagtca acttcttg 18